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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/965,825

DATE: 11/07/2001
TIME: 14:41:53

Input Set : A:\es.txt
Output Set: N:\CRF3\11072001\I965825.raw

3 <110> APPLICANT: DUSCH, Nicole
4 THOMAS, Hermann
5 THIERBACH, Georg
7 <120> TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID USING
8 CORYNEFORM BACTERIA
10 <130> FILE REFERENCE: 21354US0X
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/965,825 OV
C--> 12 <141> CURRENT FILING DATE: 2001-10-01
12 <150> PRIOR APPLICATION NUMBER: DE 10048604.5
13 <151> PRIOR FILING DATE: 2000-09-30
15 <150> PRIOR APPLICATION NUMBER: DE 10117085.8
16 <151> PRIOR FILING DATE: 2001-04-06
18 <160> NUMBER OF SEQ ID NOS: 14
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2160
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (327)..(2063)
30 <223> OTHER INFORMATION:
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34 <221> NAME/KEY: -35_signal
35 <222> LOCATION: (227)..(232)
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39 <220> FEATURE:
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48 cgaggcgacc agacaggcgt gcccacgatg tttaaatagg cgatcggtgg gcatctgtgt 120
50 ttggtttgcg cgggtcgaaa ccaaaccaga ctgcccagca acgacggaaa tcccaaaagt 180
52 gggcatccct gtttggtacc gagtacccac ccgggcctga aactccctgg caggcgggcn 240
54 aagcgtggca acaactggaa tttaagagaca caattgaagt cgcaccaagt tagccaacac 300
56 aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta 353
57 Met Ala His Ser Tyr Ala Glu Gln Leu
58 1 5
60 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401
61 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
62 10 15 20 25
64 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449
65 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
66 30 35 40
68 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 497
69 Glu Trp Val His Val Arg Asn Glu Ala Ala Ala Phe Ala Ala Gly

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70	45	50	55	
72	gca gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt			545
73	Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys			
74	60	65	70	
76	ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga			593
77	Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg			
78	75	80	85	
80	aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag			641
81	Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln			
82	90	95	100	105
84	att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag			689
85	Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys			
86	110	115	120	
88	gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa			737
89	Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu			
90	125	130	135	
92	cgc att ttg cat cac gca att cag tcc acc atg gcg ggt aaa ggt gtg			785
93	Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val			
94	140	145	150	
96	tcg gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac			833
97	Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp			
98	155	160	165	
100	ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc			881
101	Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe			
102	170	175	180	185
104	ccg gat cct act gag gct gca gca ctg gtg gag gcg att aac aac gct			929
105	Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala			
106	190	195	200	
108	aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg			977
109	Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala			
110	205	210	215	
112	cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg			1025
113	Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala			
114	220	225	230	
116	ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc			1073
117	Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly			
118	235	240	245	
120	atg tct ggc ctg ctt ggt tac gac ggc tgc gtg gat gcg tcc aat gag			1121
121	Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu			
122	250	255	260	265
124	gct gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc			1169
125	Ala Asp Leu Leu Ile Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe			
126	270	275	280	
128	ctt cct aaa gac aac gtt gcc cag gtg gat atc aac ggt gcg cac att			1217
129	Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile			
130	285	290	295	
132	ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt gat gtt gct gca			1265
133	Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala			
134	300	305	310	

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133	aca atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc	1313		
137	Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser			
138	315	320	325	
140	ttc ctt gat cggtatgcgttc aag gca cac gag cgt aag ttg agc tcg gtg	1361		
141	Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val			
142	330	335	340	345
144	gta gag acg tac aca cat aac gtc gag aag cat gtg cct att cac cct	1409		
145	Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro			
146	350	355	360	
148	gaa tac gtt gcc tct att ttg aac gag ctg gcg gat aag gat gcg gtg	1457		
149	Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val			
150	365	370	375	
152	ttt act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc	1505		
153	Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile			
154	380	385	390	
156	gag aat ccg gag gga acg cgc gac ttt gtg ggt tca ttc cgc cac ggc	1553		
157	Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly			
158	395	400	405	
160	acg atg gct aat gcg ttg cct cat gcg att ggt gcg caa agt gtt gat	1601		
161	Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala Gln Ser Val Asp			
162	410	415	420	425
164	cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt ggt ttg ggc atg	1649		
165	Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met			
166	430	435	440	
168	ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag	1697		
169	Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys			
170	445	450	455	
172	gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg	1745		
173	Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met			
174	460	465	470	
176	ctc gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat	1793		
177	Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn			
178	475	480	485	
180	ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc	1841		
181	Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr			
182	490	495	500	505
184	gat ccg aag aaa gtt cgc gag cag cta gct gag gca ttg gca tat cct	1889		
185	Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro			
186	510	515	520	
188	gga cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc	1937		
189	Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile			
190	525	530	535	
192	cca cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc	1985		
193	Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala			
194	540	545	550	
196	acc cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc	2033		
197	Thr Arg Thr Val Phe Gly Gly Val Gly Ala Met Ile Asp Leu Ala			
198	555	560	565	
200	cgt tcg aac ata agg aat att cct act cca tgatgattga tacacctgct	2083		

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201 Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
202 570      575
204 gttctcattg accgcgagcg cttaactgcc aacatttcca ggatggcagc tcacgcccgt  2143
206 gcccatgaga ttgcctc
209 <210> SEQ ID NO: 2
210 <211> LENGTH: 579
211 <212> TYPE: PRT
212 <213> ORGANISM: Corynebacterium glutamicum
214 <400> SEQUENCE: 2
216 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
217 1          5          10          15
220 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
221          20          25          30
224 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
225          35          40          45
228 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
229          50          55          60
232 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
233          65          70          75          80
236 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
237          85          90          95
240 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
241          100         105         110
244 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
245          115         120         125
248 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
249          130         135         140
252 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
253          145         150         155         160
256 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
257          165         170         175
260 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
261          180         185         190
264 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
265          195         200         205
268 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
269          210         215         220
272 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
273          225         230         235         240
276 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
277          245         250         255
280 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
281          260         265         270
284 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
285          275         280         285
288 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
289          290         295         300
292 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
293          305         310         315         320

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296	His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys			
297	325	330	335	
300	Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn			
301	340	345	350	
304	Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu			
305	355	360	365	
308	Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met			
309	370	375	380	
312	Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg			
313	385	390	395	400
316	Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro			
317	405	410	415	
320	His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala			
321	420	425	430	
324	Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr			
325	435	440	445	
328	Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser			
329	450	455	460	
332	Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu			
333	465	470	475	480
336	Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala			
337	485	490	495	
340	Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu			
341	500	505	510	
344	Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile			
345	515	520	525	
348	Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu			
349	530	535	540	
352	Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly			
353	545	550	555	560
356	Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile			
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360	Pro Thr Pro			
364	<210> SEQ ID NO: 3			
365	<211> LENGTH: 875			
366	<212> TYPE: DNA			
367	<213> ORGANISM: Corynebacterium glutamicum			
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372	accatggcggtt gtaaaagggtgt gtcgggtggta gtgattcctg gtgatatcgc taagaagac	120		
374	gcagggtgacgt gtacttatttc caattccact atttcttctg gcactcctgt ggtttccccg	180		
376	gatcctactg aggctgcacgc gctgggtggag gcgattaaaca acgctaagtc tgtcaacttg	240		
378	ttctcgccgtt cggccgtgaa gaatgctcgc ggcgcagggtgt tggagttggc ggagaagatt	300		
380	aaatcaccga tcggcatgc gctgggttgtt aagcagtaca tccagcatga gaatccgttt	360		
382	gagggtcgcca tgtctggcct gcttggttac ggcgcctgcg tggatgcgtc caatgaggcg	420		
384	gatctgctga ttcttattggg tacggatttc ccttattctg atttccttcc taaagacaac	480		
386	gttgcgcagg tggatatcaa cggtgcgcac attggtcgac gtaccacgggt gaagtatccg	540		
388	gtgaccgggtt atgttgctgc aacaatcgaa aatattttgc ctcatgtgaa ggaaaaaaaca	600		
390	gatcgttcct tccttgcgt gatgctcaag gcacacgago gtaagttgag ctcgggttga	660		

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date